# Population Genetics of the blow fly *Phormia regina* (Meigen)

John W. Whale and Christine J. Picard
Department of Biology
Indiana University-Purdue University Indianapolis

Blow flies (Diptera: Calliphoridae) are a family of flies which are associated with the decomposition of organic matter, and the many species are widely distributed across the globe inhabiting almost every ecosystem and continent, with the exception being Antarctica. For many years, biologists have been interested in these metamorphic insects with much attention in recent years with their predictable life cycle and subsequent application in death investigations. *Phormia regina* (Meigen) is a primary colonizer of carrion and is widely distributed across the United States and can be found throughout the year.

Recently, molecular techniques have been applied to a number of blow fly species, initially for identification purposes to corroborate morphological taxonomy but also as an alternative to morphology when specimens are damaged. Even more recently, population structure of these flies have been investigated, however these studies have primarily focused on pest species which infest living livestock and directly affect the agricultural economy. Here, we build upon previous analysis with AFLP markers on *P. regina* to determine the population structure of this integral species by using tetra-nucleotide microsatellite markers.

From the recently constructed draft genome of *P. regina*, several thousand tetra-nucleotide (four-base repeating sequences of DNA) were identified. Due to the high A-T content of insect DNA, repeats consisting wholly of adenine and thymine bases were discarded. From the remaining tetra-repeats, 14 were chosen for initial analysis to determine their polymorphic nature; from here six were selected for genotypic analysis.

More than 200 different *P. regina* individuals belonging to 27 populations collected from across the contiguous United States have been genotyped across these six tetra-nucleotide loci. Five loci possess ≥30 different alleles, while the sixth appears to be fairly conserved with eight different alleles. Heterozygosity exhibited between these populations is uniform (0.5-0.8) while inbred lab colonies exhibit an increase in homozygosity from their ancestral population. Further analyses are to be performed in order to determine the population structure and geography-genetic relationships of these flies.

**Key words:** *Phormia regina*, microsatellites, population genetics